

*Friedman*

**RAW SEQUENCE LISTING**  
**ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH

#1 #4  
**RECEIVED**

SEP 08 2000

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form: **TECH CENTER 1600/2900**

Application Serial Number: 09/544,934

Source: 1655

Date Processed by STIC: 8/31/2000

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25. Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/544,934

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 J Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>  
sections for Artificial or Unknown sequences.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
<400> sequence id number  
000
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism      Sequence(s)        are missing this mandatory field or its response.  
(NEW RULES)
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

27. Fredman

See item 5 on Ena summary sheet

1655

Does Not Comply  
Corrected Diskette Needed

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/544,934

DATE: 09/05/2000  
TIME: 11:42:57

Input Set : A:\PTO.txt  
Output Set : N:\CRF3\09052000\I544934.raw

SEQUENCE LISTING

E--> 42 (A) Vineet Kohli  
E--> 43 (B) Reg. 37,003  
4 (1) GENERAL INFORMATION:  
6 (i) APPLICANT: Henrik Stender  
7 Kaare Lund  
8 Tina Anderson Hollerup  
10 (ii) TITLE OF INVENTION: Novel Process For The Detection of Mycobacteria  
12 (iii) NUMBER OF SEQUENCES: 123  
14 (iv) CORRESPONDENCE ADDRESS:  
16 (A) ADDRESSEE: GRAHAM & JAMES LLP  
E--> 17 (B) STREET: ← please insert colon after STREET;  
18 (C) CITY: New York otherwise, response  
19 (D) STATE: New York will not  
20 (E) COUNTRY: USA appear in  
21 (F) ZIP: 10022 processed  
23 (v) COMPUTER READABLE FORM:  
24 (A) MEDIUM TYPE: Floppy disk 3.5 inch  
25 (B) COMPUTER: IBM PC compatible  
26 (C) OPERATING SYSTEM: ASCII  
27 (D) SOFTWARE: Microsoft Word  
29 (vi) CURRENT APPLICATION DATA:  
30 (A) APPLICATION NUMBER: US/09/544,934  
31 (B) FILING DATE: 07-Apr-2000  
33 (vii) PRIOR APPLICATION DATA:  
34 (A) APPLICATION NUMBER: 60/028,392  
35 (B) FILING DATE: 15-Oct-96  
36 (A) APPLICATION NUMBER: 60/029,595  
37 (B) FILING DATE: 23-Oct-96  
38 (A) APPLICATION NUMBER: 05/05/97 not an application number  
39 (B) FILING DATE: 08-May-97  
C--> 41 (viii) ATTORNEY/AGENT INFORMATION:  
47 (ix) TELECOMMUNICATION INFORMATION:  
48 (A) TELEPHONE: (212) 848-1065  
49 (B) TELEFAX: (212) 688-2449

There are at  
top of page  
because no  
readings shown  
under  
(viii) ATTORNEY/AGENT  
INFORMATION:  
Please insert  
readings, or  
shown below:

(A) NAME:  
(B) REGISTRATION NUMBER?

ERRORED SEQUENCES

226 (2) INFORMATION FOR SEQ ID NO: 15:  
228 (i) SEQUENCE CHARACTERISTICS: 14  
229 (A) LENGTH: 15 basepairs  
230 (B) TYPE: nucleic acid basepairs  
231 (C) STRANDEDNESS: single  
232 (D) TOPOLOGY: linear  
C--> 234 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
E--> 236 GATTCGTAC GGGC 15 14

RECEIVED

SEP 08 2000

TECH CENTER 1600/2900

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/544,934

DATE: 09/05/2000  
 TIME: 11:42:57

Input Set : A:\PTO.txt  
 Output Set: N:\CRF3\09052000\I544934.raw

606 (2) INFORMATION FOR SEQ ID NO: 44:  
 608 (i) SEQUENCE CHARACTERISTICS: 14  
 609 (A) LENGTH: 15 basepairs  
 610 (B) TYPE: nucleic acid basepairs  
 611 (C) STRANDEDNESS: single  
 612 (D) TOPOLOGY: linear  
 C--> 614 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:  
 E--> 616 GATCAATGCT CGGT (15) 14  
 1119 (2) INFORMATION FOR SEQ ID NO: 83:  
 1121 (i) SEQUENCE CHARACTERISTICS:  
 1122 (A) LENGTH: 15 basepairs  
 1123 (B) TYPE: nucleic acid basepairs  
 1124 (C) STRANDEDNESS: single  
 1125 (D) TOPOLOGY: linear  
 OK 1127 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:  
 1129 AGATTGCCCA CGGT 15  
 E--> 1132 (2) INFORMATION FOR SEQ ID NO: 84  
 E--> 1134 (i) SEQUENCE CHARACTERISTICS:  
 E--> 1135 (A) LENGTH: 15 basepairs  
 E--> 1136 (B) TYPE: nucleic acid basepairs  
 E--> 1137 (C) STRANDEDNESS: single  
 E--> 1138 (D) TOPOLOGY: linear  
 E--> 1140 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:  
 E--> 1142 AATCCGAGAA AACC 15  
 E--> 1145 (2) INFORMATION FOR SEQ ID NO: 85:  
 1147 (i) SEQUENCE CHARACTERISTICS:  
 1148 (A) LENGTH: 15 basepairs  
 1149 (B) TYPE: nucleic acid basepairs  
 1150 (C) STRANDEDNESS: single  
 1151 (D) TOPOLOGY: linear  
 OK 1153 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:  
 1155 GCATTACCCG CTGC 15

(2) INFORMATION FOR SEQ ID NO: 84:

error affects sequence appearance  
 (reason for bolded lines)

VERIFICATION SUMMARY  
 PATENT APPLICATION: US/09/544,934

DATE: 09/05/2000  
 TIME: 11:42:58

Input Set : A:\PTO.txt  
 Output Set: N:\CRF3\09052000\I544934.raw

L:17 M:220 C: Keyword misspelled or invalid format, [(B) STREET:]  
 L:17 M:220 C: Keyword misspelled or invalid format, Poss data loss, (B) STREET:  
 L:29 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]  
 L:29 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]  
 L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
 L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
 L:41 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]  
 L:42 M:243 E: Alpha Header Field expected, Data=[(A) Vineet Kohli], General Header Line Not Processed!  
 L:42 M:243 E: Alpha Header Field expected, Data=[(B) Reg. 37,003], General Header Line Not Processed!  
 L:43 M:243 E: Alpha Header Field missing, [(B) STREET:] Value not provided  
 L:17 M:200 E: Mandatory Header Field missing, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:59 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:71 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:83 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:95 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:107 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:119 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:131 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:143 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:156 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:169 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:182 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:195 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:208 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:221 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:234 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:236 M:254 E: No. of Bases conflict, Input:15 Counted:14 SEQ:15  
 L:236 M:204 E: No. of Bases differ, LENGTH:Input:15 Counted:14 SEQ:15  
 L:247 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:260 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:273 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:286 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:299 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:312 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:325 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:338 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:351 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:364 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:378 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:391 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:404 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:417 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:430 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:443 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:456 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:470 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:483 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:496 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:509 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]

VERIFICATION SUMMARY  
 PATENT APPLICATION: US/09/544,934

DATE: 09/05/2000  
 TIME: 11:42:58

Input Set : A:\PTO.txt  
 Output Set: N:\CRF3\09052000\I544934.raw

L:522 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:535 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:548 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:562 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:575 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:588 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:601 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]  
 L:616 M:254 E: No. of Bases conflict, Input:15 Counted:14 SEQ:44  
 L:616 M:204 E: No. of Bases differ, LENGTH:Input:15 Counted:14 SEQ:44  
 L:1132 M:254 E: No. of Bases conflict, Input:84 Counted:24 SEQ:83  
 L:1132 M:320 E: (1) Wrong Nucleic Acid Designator, 15  
 L:1134 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3  
 L:1134 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:1135 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
 L:1135 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4  
 L:1135 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:1136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
 L:1136 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5  
 L:1136 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:1137 M:336 W: Invalid Amino Acid Number in Coding Region, NUMBER OF INVALID KEYS:3  
 L:1137 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3  
 L:1137 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 L:1138 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:0  
 L:1138 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3  
 L:1138 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
 M:254 Repeated in SeqNo=83  
 L:1140 M:320 E: (1) Wrong Nucleic Acid Designator, 22  
 L:1142 M:204 E: No. of Bases differ, LENGTH:Input:15 Counted:86 SEQ:83  
 L:1145 M:216 E: (34) Seq.#s missing, 86 thru 84  
 L:1660 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:123  
 L:12 M:203 E: No. of Seq. differs, : Input 123, Counted 122